

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/436,339ADATE: 07/02/98
TIME: 14:54:25

INPUT SET: S3203.raw

#19

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

- (i) APPLICANT: Papayannopoulou, Thalia (USA only)
Board of Regents, U.
Washington (except USA)
- (ii) TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
CELLS
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: c/o FISH & NEAVE
(B) STREET: 1251 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10020
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/436,339
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/463,128
(B) FILING DATE: 05-JUN-1995

(A) APPLICATION NUMBER: PCT/US93/11060
(B) FILING DATE: 11-11-1993

(A) APPLICATION NUMBER: US 07/977,702
(B) FILING DATE: 13-NOV-1992
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Haley Jr., James F.
(B) REGISTRATION NUMBER: 27,794
(C) REFERENCE/DOCKET NUMBER: B173CIP

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/436,339ADATE: 07/02/98
TIME: 14:54:27

INPUT SET: S3203.raw

47
48 (ix) TELECOMMUNICATION INFORMATION:
49 (A) TELEPHONE: (212) 596-9000
50 (B) TELEFAX: (212) 596-9090
51
52
53 (2) INFORMATION FOR SEQ ID NO:1:
54
55 (i) SEQUENCE CHARACTERISTICS:
56 (A) LENGTH: 360 base pairs
57 (B) TYPE: nucleic acid
58 (C) STRANDEDNESS: single
59 (D) TOPOLOGY: linear
60
61
62
63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65 GTCAAACTGC AGCAGTCTGG GGCAGAGCTT GTGAAGCCAG GGCCTCAGT CAAGTTGTCC 60
66
67 TGCACAGCTT CTGGCTTCAA CATTAAAGAC ACCTATATGC ACTGGGTGAA GCAGAGGCCT 120
68
69 GAACAGGGCC TGGAGTGGAT TGAAGGATT GATCCTGCGA GTGGCGATAC TAAATATGAC 180
70
71 CCGAAGTTCC AGGTCAAGGC CACTATTACA GCGGACACGT CCTCCAACAC AGCCTGGCTG 240
72
73 CAGCTCAGCA GCCTGACATC TGAGGACACT GCCGTCTACT ACTGTGCAGA CGGAATGTGG 300
74
75 GTATCAACGG GATATGCTCT GGAATTCTGG GGCCAAGGGA CCACGGTCAC CGTCTCCTCA 360
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77
78 (2) INFORMATION FOR SEQ ID NO:2:
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80 (i) SEQUENCE CHARACTERISTICS:
81 (A) LENGTH: 318 base pairs
82 (B) TYPE: nucleic acid
83 (C) STRANDEDNESS: single
84 (D) TOPOLOGY: linear
85
86
87
88 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
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91
92 ATAACCTGCA AGGCCAGTCA GAGTGTGACT AATGATGTAG CTTGGTACCA ACAGAAGCCA 120
93
94 GGGCAGTCTC CTAACTGCT GATATATTAT GCATCCAATC GCTACACTGG AGTCCCTGAT 180
95
96 CGCTTCACTG GCAGTGGATA TGGGACGGAT TTCACTTTCA CCATCAGCAC TGTGCAGGCT 240
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98 GAAGACCTGG CAGTTTATTT CTGTCAGCAG GATTATAGCT CTCCGTACAC GTTCGGAGGG 300
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/436,339A

DATE: 07/02/98
TIME: 14:54:29

INPUT SET: S3203.raw

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100 GGGACCAAGC TGGAGATC
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102 (2) INFORMATION FOR SEQ ID NO:3:
103
104 (i) SEQUENCE CHARACTERISTICS:
105 (A) LENGTH: 429 base pairs
106 (B) TYPE: nucleic acid
107 (C) STRANDEDNESS: single
108 (D) TOPOLOGY: linear
109
110
111 (ix) FEATURE:
112 (A) NAME/KEY: sig_peptide
113 (B) LOCATION: 1..57
114
115 (ix) FEATURE:
116 (A) NAME/KEY: mat_peptide
117 (B) LOCATION: 58..429
118
119 (ix) FEATURE:
120 (A) NAME/KEY: CDS
121 (B) LOCATION: 1..429
122
123 (ix) FEATURE:
124 (A) NAME/KEY: misc_feature
125 (B) LOCATION: 1
126 (D) OTHER INFORMATION: /note= "pMDR1019 insert: Stage 1
127 heavy chain variable region"
128
129
130 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
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133 Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
134 -19 -15 -10 -5
135
136 GCC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA 96
137 Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
138 1 5 10
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140 CCT AGC CAG ACC CTG AGC CTG ACC TGC ACC GTG TCT GGC TTC AAC ATT 144
141 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Asn Ile
142 15 20 25
143
144 AAA GAC ACC TAT ATG CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT 192
145 Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
146 30 35 40 45
147
148 GAG TGG ATT GGA AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC 240
149 Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
150 50 55 60
151
152 CCG AAG TTC CAG GTC AGA GTG ACA ATG CTG GTA GAC ACC AGC AAG AAC 288

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/436,339A

DATE: 07/02/98
TIME: 14:54:31

INPUT SET: S3203.raw

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153 Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn
154      65      70      75
155
156 CAG TTC AGC CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC      336
157 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
158      80      85      90
159
160 TAT TAT TGT GCA GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC      384
161 Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
162      95      100      105
163
164 TTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GAG TCC      429
165 Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
166 110      115      120
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169 (2) INFORMATION FOR SEQ ID NO:4:
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171 (i) SEQUENCE CHARACTERISTICS:
172 (A) LENGTH: 143 amino acids
173 (B) TYPE: amino acid
174 (D) TOPOLOGY: linear
175
176 (ii) MOLECULE TYPE: protein
177
178 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
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180 Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
181 -19      -15      -10      -5
182
183 Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
184      1      5      10
185
186 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Asn Ile
187 15      20      25
188
189 Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
190 30      35      40      45
191
192 Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
193      50      55      60
194
195 Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn
196      65      70      75
197
198 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
199      80      85      90
200
201 Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
202      95      100      105
203
204 Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
205 110      115      120

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/436,339ADATE: 07/02/98
TIME: 14:54:33

INPUT SET: S3203.raw

206
207 (2) INFORMATION FOR SEQ ID NO:5:
208
209 (i) SEQUENCE CHARACTERISTICS:
210 (A) LENGTH: 386 base pairs
211 (B) TYPE: nucleic acid
212 (C) STRANDEDNESS: single
213 (D) TOPOLOGY: linear
214
215
216 (ix) FEATURE:
217 (A) NAME/KEY: sig_peptide
218 (B) LOCATION: 1..57
219
220 (ix) FEATURE:
221 (A) NAME/KEY: mat_peptide
222 (B) LOCATION: 58..384
223
224 (ix) FEATURE:
225 (A) NAME/KEY: CDS
226 (B) LOCATION: 1..384
227
228 (ix) FEATURE:
229 (A) NAME/KEY: misc_feature
230 (B) LOCATION: 1
231 (D) OTHER INFORMATION: /note= "pBag190 insert: VK1 (DQL)
232 light chain variable region"
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234
235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
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237 ATG GGT TGG TCC TGC ATC ATC CTG TTC CTG GTT GCT ACC GCT ACC GGT 48
238 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
239 -19 -15 -10 -5
240
241 GTT CAC TCC GAC ATC CAG CTG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96
242 Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
243 1 5 10
244
245 AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AGT GTG 144
246 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
247 15 20 25
248
249 ACT AAT GAT GTA GCT TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG 192
250 Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
251 30 35 40 45
252
253 CTG CTG ATC TAC TAT GCA TCC AAT CGC TAC ACT GGT GTG CCA AGC AGA 240
254 Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg
255 50 55 60
256
257 TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC 288
258 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/436,339A

DATE: 07/02/98
TIME: 14:54:35

INPUT SET: S3203.raw

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